PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:
  O. FAMODU ET AL.

CASE NO.: BB-1270

APPLICATION NO.:   09/831,683

CONFIRMATION NO.: 7062

GROUP ART UNIT: UNKNOWN

EXAMINER: UNKNOWN

I. A. FILING DATE: 11/09/1999

FOR: PLANT AMINOACYL-TRNA SYNTHETASES

STATEMENT UNDER 37 CFR 1.825(d), 1.821(f), and 1.821(g)

Commissioner for Patents
Box PCT
Washington, D.C. 20231

Sir:

The submission of the substitute Sequence Listing filed concurrently herewith does not include new matter.

The copy of substitute Sequence Listing in computer readable form filed concurrently herewith is identical to that currently on file, is the same as the paper copy of the substitute Sequence Listing filed concurrently herewith, and does not include new matter.

Respectfully submitted,

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Telephone: 302-992-4929
Facsimile: 302-892-1026

Dated: *14 February 2003*

SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company

<120> Plant Aminoacyl-tRNA Synthetases

<130> BB1270

<140> US/09/831,683
<141> 2001-05-10

<150> 60/107,789
<151> 1998-11-10

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His Gln Ile Pro Leu Ile Val Val Lys Ser Asp Gly Gly Phe Asn Tyr
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            195   200   205

Ala His Ala Arg Ile Cys Ser Ile Ile Arg Lys Ser Asn Lys Asn Val
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225   230   235   240

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Glu Val Ser Lys Pro Gly Phe Gly Asp Tyr Gln Cys Asn Asn Ala Met
         35                  40                  45

Ser Val Phe Ser Arg Ile Arg Gly Ser Ala Thr Asn Phe Arg Asn Pro
     50                  55                  60

Met Ala Val Gly Gln Ala Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile
 65                  70                  75                  80

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3

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Gly Met Leu Ile Glu Phe Leu Phe Glu Gln Phe Pro Asp Trp Glu Asp
                180                 185                 190

Val Gly Asn Gln Ala Val Gly Asp Leu Gln Ser Phe Tyr Lys Ala Ser
                195                 200                 205

Lys Lys Arg Phe Asp Asp Asp Pro Asp Phe Lys Glu Arg Ala Arg Gln
    210                 215                 220

Ala Val Val Arg Leu Gln Gly Gly Glu Asp Lys Tyr Arg Ala Ala Trp
225                 230                 235                 240

Lys Lys Ile Cys Gln Ile Ser Arg Met Glu Phe Asp Leu Val Tyr Lys
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Arg Leu Asn Val Lys Leu Glu Glu Lys Gly Glu Ser Phe Tyr Asn Pro
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Tyr Ile Pro Pro Val Leu Glu Glu Leu Thr Asn Lys Gly Leu Ile Val
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Glu Ser Lys Gly Ala Arg Val Ile Phe Val Glu Asp His Pro Leu Ile
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Val Ile Lys Gln Asp Gly Gly Phe Asn Tyr Ala Ser Thr Asp Leu Ala
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Ser Glu Ala Ile Gly Tyr Gly Ala Val Lys Tyr Ser Asp Leu Lys Asn
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4

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Leu Ile Gln Phe Thr Glu Val Val Glu Gln Ala Cys Ala Asp Leu Gln
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Pro His Arg Leu Cys Asp Tyr Leu Tyr Ser Leu Ser Leu Thr Phe Ser
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Lys Phe Tyr Thr Asn Cys Gln Val Val Gly Ser Pro Glu Glu Thr Ser
545   550   555   560

Arg Leu Leu Leu Cys Glu Ala Thr Gly Ile Ile Met Arg Gln Cys Phe
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         Gln His Phe Asp Met Leu Phe Lys Ala Tyr Arg Arg Ala Gly Trp Leu
             50                  55                  60

         Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly
         65                  70                  75                      80

         Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Ser Ser Glu
                         85                  90                  95

         Val Val Arg Leu Val Asp Leu Leu Asp Glu Ala Lys Arg Arg Cys Lys
                     100                 105                 110

         Ile Ala Ile Leu Glu Arg Asp Thr Thr Lys Asp Trp Ser Glu Glu Glu
                     115                 120                 125

         Ile Glu Lys Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala
                 130                 135                 140

         Asp Leu Lys Ile Asn Arg Leu Thr Asn Tyr Thr Phe Asn Phe Asp Gln
         145                 150                 155                     160

         Met Leu Asn Asp Lys Gly Asn Thr Ala Val Tyr Leu Leu Tyr Ala His
                         165                 170                 175

         Ala Arg Ile Cys Ser Ile Ile Arg Lys Ser Gly Lys Asp Ile Glu Glu
                     180                 185                 190

         Val Lys Arg Asn Gly Lys Ile Val Leu Asp His Glu Asp Glu Arg Ala
                 195                 200                 205

         Leu Gly Leu His Leu Leu Gln Phe Pro Glu Val Phe Glu Glu Ala Cys
             210                 215                 220

         Thr Asn Leu Leu Pro Asn Phe Leu Cys Glu Tyr Leu Tyr Asn Leu Ala
         225                 230                 235                     240

         Glu Ile Phe Thr Lys Lys Phe Tyr Ala Asn Cys Gln Val Val Gly Ser
                         245                 250                 255

         Pro Glu Glu Thr Ser Arg Leu Leu Leu Cys Glu Ala Thr Val Thr Val
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             20                  25                  30

Gly Ala Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg
         35                  40                  45

Leu Gly Asp Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu
     50                  55                  60

Leu Gln Arg Leu Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Glu
 65                  70                  75                  80

Glu Leu Glu Gln Thr Ser Lys Ala Val Gly Tyr Gly Ala Val Lys Tyr
                 85                  90                  95

Ala Asp Leu Lys Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Asp
            100                 105                 110

Gln Met Leu Ser Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala
            115                 120                 125

His Ala Arg Ile Cys Ser Ile Ile Arg Lys Ser Asn Met Asp Val Glu
        130                 135                 140

Glu Leu Lys Val Ser Gly Asn Ile Ser Leu Ala His Pro Asp Glu Arg
145                 150                 155                 160

Val Leu Gly Leu Tyr Leu Ile Arg Tyr Ala Glu Ile Val Glu Glu Ala
                165                 170                 175

Cys Thr Asn Leu Leu Pro Ser Val Leu Cys Glu Tyr Leu Tyr Asn Leu
            180                 185                 190

Ser Glu Met Phe Thr Arg Phe Tyr Thr Asn Cys Gln Val Val Gly Ser
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7

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cgcttagcta ggcatggtga ccacctttg ggcacatgga attcctgagt tgacaatgag 2400
tattgttgca ttgtacactt taatattgta ctgtgattag ctttactcg cggtggatgt 2460
ctttcaccgc tagatggcca gaggcatatc ctgccaacca agcagagcag ccattttgat 2520
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<210> 10
<211> 715
<212> PRT
<213> Zea mays

<400> 10

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Met Glu Ala Ala Leu Ser Phe Ser Lys Asp Ser Pro Pro Ile Ser Ile
  1               5                  10                  15

Ile Cys Ala Ala Lys Leu Val Gly Leu Pro Leu Thr Ile Asn His Ser
              20                  25                  30

Leu Ala Ala Gly Ser Ala Pro Thr Leu Gln Phe Ala Ser Gly Glu Ser
          35                  40                  45

Leu His Gly Val Asn Pro Ile Ile Leu Tyr Ile Ala Arg Gly Ala Ser
      50                  55                  60

Ile Ala Ser Leu Ser Gly Lys Asn Asp Ile Glu Phe Gly His Val Val
 65               70                  75                      80

Glu Trp Leu Glu Tyr Ala Pro Thr Phe Leu Ser Gly Ser Glu Phe Glu
              85                  90                  95

Asn Ala Cys Leu Phe Val Asp Gly Phe Leu Ala Ser Arg Thr Phe Leu
             100                 105                 110

Val Gly His Gly Leu Thr Ile Ala Asp Ile Ala Val Trp Ser Asn Leu
         115                 120                 125

Ala Gly Ile Gly Gln Arg Trp Glu Ser Leu Arg Lys Ser Lys Lys Tyr
         130                 135                 140

Gln Asn Leu Val Arg Trp Phe Asn Ser Ile Asp Ser Glu Tyr Lys Glu
145                 150                 155                 160

Ala Leu Asn Glu Val Val Ala Ala Phe Val Gly Lys Arg Gly Ile Gly
             165                 170                 175

Lys Ser Pro Ala Pro Ser Leu Lys Glu Lys Val His Asp Ser Lys Asp
             180                 185                 190

Pro Ser Ala Pro Glu Val Asp Leu Pro Gly Ala Lys Val Gly Lys Val
         195                 200                 205

Cys Val Arg Phe Ala Pro Glu Pro Ser Gly Tyr Leu His Ile Gly His
     210                 215                 220

Ala Lys Ala Ala Leu Leu Asn Lys Tyr Phe Ala Glu Arg Tyr Gln Gly
225                 230                 235                 240

Arg Leu Ile Val Arg Phe Asp Asp Thr Asn Pro Ser Lys Glu Ser Asn
             245                 250                 255

Glu Phe Val Glu Asn Leu Leu Lys Asp Ile Glu Thr Leu Gly Ile Lys
             260                 265                 270

Tyr Asp Ala Val Thr Tyr Thr Ser Asp Tyr Phe Pro Lys Leu Met Glu
         275                 280                 285

Met Ala Glu Ser Leu Ile Lys Gln Gly Lys Ala Tyr Ile Asp Asp Thr
290                 295                 300

Pro Lys Glu Gln Met Arg Lys Glu Arg Met Asp Gly Ile Glu Ser Arg
305                 310                 315                 320
```

9

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Cys Arg Asn Asn Thr Val Glu Glu Asn Leu Ser Leu Trp Lys Glu Met
            325             330             335

Val Asn Gly Thr Glu Arg Gly Met Gln Cys Cys Val Arg Gly Lys Leu
            340             345             350

Asp Met Gln Asp Pro Asn Lys Ser Leu Arg Asp Pro Val Tyr Tyr Arg
            355             360             365

Cys Asn Thr Asp Pro His His Arg Val Gly Ser Lys Tyr Lys Val Tyr
    370             375             380

Pro Thr Tyr Asp Phe Ala Cys Pro Phe Val Asp Ala Leu Glu Gly Val
385                 390             395                 400

Thr His Ala Leu Arg Ser Ser Glu Tyr His Asp Arg Asn Ala Gln Tyr
                405             410             415

Tyr Arg Ile Leu Gln Asp Met Gly Leu Arg Arg Val Glu Ile Tyr Glu
            420             425             430

Phe Ser Arg Leu Asn Met Val Tyr Thr Leu Leu Ser Lys Arg Lys Leu
            435             440             445

Leu Trp Phe Val Gln Asn Lys Lys Val Glu Asp Trp Thr Asp Pro Arg
    450             455             460

Phe Pro Thr Val Gln Gly Ile Val Arg Arg Gly Leu Lys Val Glu Ala
465             470             475             480

Leu Ile Gln Phe Ile Leu Gln Gln Gly Ala Ser Lys Asn Leu Asn Leu
            485             490             495

Met Glu Trp Asp Lys Leu Trp Thr Ile Asn Lys Lys Ile Ile Asp Pro
            500             505             510

Val Cys Ala Arg His Thr Ala Val Leu Lys Asp Gln Arg Val Ile Phe
            515             520             525

Thr Leu Thr Asn Gly Pro Glu Glu Pro Phe Val Arg Ile Leu Pro Arg
    530             535             540

His Lys Lys Phe Glu Gly Ala Gly Lys Lys Ala Thr Thr Phe Ala Asn
545             550             555             560

Arg Ile Trp Leu Asp Tyr Ala Asp Ala Ala Ile Asn Lys Gly Glu
            565             570             575

Glu Val Thr Leu Met Asp Trp Gly Asn Ala Ile Val Lys Glu Ile Lys
            580             585             590

Val Glu Ser Gly Val Ile Thr Glu Leu Val Gly Glu Leu His Leu Glu
            595             600             605

Gly Ser Val Lys Thr Thr Lys Leu Lys Ile Thr Trp Leu Ala Asp Ile
    610             615             620

Glu Glu Leu Val Pro Leu Ser Leu Val Glu Phe Asp Tyr Leu Ile Ser
625             630             635             640
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10

Lys Lys Lys Leu Glu Glu Asp Glu Asp Phe Leu Asp Asn Leu Asn Pro
                645   650   655

Cys Thr Arg Arg Glu Ile Pro Ala Leu Gly Asp Ala Asn Met Arg Asn
            660   665   670

Ile Lys Arg Gly Glu Ile Ile Gln Leu Glu Arg Lys Gly Tyr Tyr Arg
        675   680   685

Cys Asp Ala Pro Phe Ile Arg Ser Ser Lys Pro Val Val Leu Phe Ala
    690   695   700

Ile Pro Asp Gly Arg Gln Gln Ala Ser Leu Ser
705   710   715

<210> 11
<211> 1920
<212> DNA
<213> Oryza sativa

<220>
<221> unsure
<222> (139)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (238)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (431)
<223> n = A, C, G or T

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tccgcctccg cctcggcgnc accggacggc gccggcggcc cggtgcgggc ccgttcgcgc 180
cgtcgccgac ggcaacctcc acgtcggcgg cgcccgcacc gcgcacttca actacctntt 240
cgcgcggtcc aaggggggca agttcgtgct ccgcatcgag gacaccgact tcgagaggtc 300
caccaagaag tccgaggagg ccgtgctcag tgacctcgcc tggctcggcc ttgactggga 360
cgaaggcccg gatgtcggtg gggaatatgg gcccgatcgc cagtccgagc gcaattcgat 420
gtacaaacag natgccgaga agctgatgga gtctggggca gtctatcagt gcttttactc 480
cagtgaggga cttgaacaga tgaaggaaac tgcaagcaga tgcaaccttc cacctgtata 540
cattggcaag tggggggactg cttcagatgc agaaatacaa caggagttag agaaggggac 600
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gttcttcacc attgatgacc tagtggaaaa attcactata aatcgtgtca caaaagtgg 1080
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cactgatgct gacgcagccc tttcaaacct gttgtcgtat cccctccatg ctacattaag 1320
cagtgatgaa gctaaatctg tggtgcaaga caagctttct gaggttgcat caggactcat 1380
ttctgcttat gatagcggtg aactttgtca agcactagct gagggccgtg atggttggca 1440
gaagtgggtg aaaattttttg gcaaatcact aaagaaag ggaaagtcac tctttatgcc 1500

11

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catacacaaa gccggcacct gtggagcggt cactcagcaa tccggtttcg taaatctcga 1620
cgagaggttc agaatcctga aggaggtgga gtgggagtca ctggtacagg agcaagagtc 1680
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gagtttttgt tttctgtaat actccactat aaagcatagg atatgttcca ttttactacc 1800
catttctaca gttgtgagga aactatagtt tcggttttct gtagttaata aagcggaatt 1860
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<210> 12
<211> 555
<212> PRT
<213> Oryza sativa

<220>
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<222> (130)
<223> Xaa = ANY AMINO ACID

<400> 12

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 1               5                  10                  15

His Leu Arg Arg Pro Ser Pro Ser Ala Pro Pro Pro Pro Pro Arg Arg
            20                  25                  30

His Arg Thr Ala Pro Ala Ala Arg Cys Gly Pro Val Arg Ala Val Ala
        35                  40                  45

Asp Gly Asn Leu His Val Gly Gly Ala Arg Thr Ala His Phe Asn Tyr
    50                  55                  60

Leu Phe Ala Arg Ser Lys Gly Gly Lys Phe Val Leu Arg Ile Glu Asp
 65                  70                  75                  80

Thr Asp Phe Glu Arg Ser Thr Lys Lys Ser Glu Glu Ala Val Leu Ser
                85                  90                  95

Asp Leu Ala Trp Leu Gly Leu Asp Trp Asp Glu Gly Pro Asp Val Gly
            100                 105                 110

Gly Glu Tyr Gly Pro Asp Arg Gln Ser Glu Arg Asn Ser Met Tyr Lys
            115                 120                 125

Gln Xaa Ala Glu Lys Leu Met Glu Ser Gly Ala Val Tyr Gln Cys Phe
    130                 135                 140

Tyr Ser Ser Glu Gly Leu Glu Gln Met Lys Glu Thr Ala Ser Arg Cys
145                 150                 155                 160

Asn Leu Pro Pro Val Tyr Ile Gly Lys Trp Gly Thr Ala Ser Asp Ala
                165                 170                 175

Glu Ile Gln Gln Glu Leu Glu Lys Gly Thr Pro Tyr Thr Tyr Arg Phe
            180                 185                 190

Arg Val Pro Lys Glu Gly Ser Leu Lys Ile Asn Asp Leu Ile Arg Gly
            195                 200                 205

Glu Val Ser Trp Asn Leu Asp Thr Leu Gly Asp Phe Val Ile Met Arg
    210                 215                 220
```

```
Ser Asn Gly Gln Pro Val Tyr Asn Phe Cys Val Thr Val Asp Asp Ala
225             230             235             240

Thr Met Arg Ile Ser His Val Ile Arg Ala Glu Glu His Leu Pro Asn
            245             250             255

Thr Leu Arg Gln Ala Leu Ile Tyr Lys Ala Leu Gly Phe Pro Met Pro
        260             265             270

Ser Phe Ala His Val Ser Leu Ile Leu Ala Pro Asp Arg Ser Lys Leu
    275             280             285

Ser Lys Arg His Gly Ala Thr Ser Val Gly Gln Tyr Lys Glu Met Gly
    290             295             300

Tyr Leu Pro Gln Ala Met Val Asn Tyr Leu Ala Leu Leu Gly Trp Gly
305             310             315             320

Asp Gly Thr Glu Asn Glu Phe Phe Thr Ile Asp Asp Leu Val Glu Lys
            325             330             335

Phe Thr Ile Asn Arg Val Asn Lys Ser Gly Ala Val Phe Asp Ala Val
            340             345             350

Lys Leu Lys Trp Met Asn Gly Gln His Leu Arg Ser Phe Pro Pro Asp
        355             360             365

Val Leu Ile Lys Ser Phe Glu Asp Arg Trp Lys Asp Thr Gly Ile Leu
    370             375             380

Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu Leu Leu Lys
385             390             395             400

Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Ala Leu Ser Asn Leu
            405             410             415

Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu Ala Lys Ser
            420             425             430

Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu Ile Ser Ala
        435             440             445

Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly Arg Asp Gly
    450             455             460

Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys Arg Lys Gly
465             470             475             480

Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly Lys Leu His
            485             490             495

Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys Ala Gly Thr
            500             505             510

Cys Gly Ala Val Thr Gln Gln Ser Gly Phe Val Asn Leu Asp Glu Arg
    515             520             525

Phe Arg Ile Leu Lys Glu Val Glu Trp Glu Ser Leu Val Gln Glu Gln
    530             535             540

Glu Ser Pro Ala Glu Thr Ala Val Pro Ala Ser
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<210> 13
<211> 731
<212> DNA
<213> Glycine max

<400> 13
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ctcccaccgg aaacctccac gtcggcggtg cccgaacggc cctcttcaac tacttgttcg 240
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caagggagtc tgaggaggcc atgctcaaag atctttcttg gcttggactt gattgggatg 360
aagggcctgg tgttggaggg gattatggtc cttataggca gtctgatagg aattctttat 420
acaagcaatt gcggataac ctacaccaat ccggtcatgt ttatcgctgc ttctgttcta 480
atgaggaact agagaaaatg aaggaggatg ctaaactaaa gcaactgcct ccagtgtaca 540
caggtaaatg ggccagtgca acaaatgagg aagtagaaga agagctagca aaaggaactc 600
cttacactta ccggttccga gtccctaaag gaagtttaaa aattaatgat caaatacgag 660
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agcctgttta t   731

<210> 14
<211> 404
<212> PRT
<213> Glycine max

<400> 14
Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly
  1   5   10   15

Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly
             20   25   30

Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Ser Thr
         35   40   45

Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu
     50   55   60

Asp Trp Asp Glu Gly Pro Gly Val Gly Gly Asp Tyr Gly Pro Tyr Arg
 65   70   75   80

Gln Ser Asp Arg Asn Ser Leu Tyr Lys Gln Phe Ala Asp Asn Leu His
                 85   90   95

Gln Ser Gly His Val Tyr Arg Cys Phe Cys Ser Asn Glu Glu Leu Glu
             100   105   110

Lys Met Lys Glu Asp Ala Lys Leu Lys Gln Leu Pro Pro Val Tyr Thr
         115   120   125

Gly Lys Trp Ala Ser Ala Thr Asn Glu Glu Val Glu Glu Glu Leu Ala
     130   135   140

Lys Gly Thr Pro Tyr Thr Tyr Arg Phe Arg Val Pro Lys Gly Ser Leu
145   150   155   160

Lys Ile Asn Asp Gln Ile Arg Gly Glu Val Ser Trp Asn Leu Asp Thr
                 165   170   175

```
Leu Gly Asp Phe Val Ile Met Arg Ser Asn Gly Gln Pro Val Tyr Asn
            180                 185             190

Phe Cys Val Thr Val Asp Asp Ala Thr Met Ala Ile Ser His Val Ile
            195                 200             205

Arg Ala Glu Glu His Leu Pro Asn Thr Leu Arg Gln Ala Leu Ile Tyr
    210                 215                 220

Lys Ala Leu Gly Phe Pro Met Pro His Phe Ala His Val Ser Leu Ile
225                 230                 235                 240

Leu Ala Pro Asp Arg Ser Lys Leu Ser Lys Arg His Gly Ala Thr Ser
            245                 250                 255

Val Gly Gln Phe Arg Asp Met Gly Tyr Leu Pro Gln Ala Met Val Asn
            260                 265                 270

Tyr Leu Ala Leu Leu Gly Trp Gly Asp Gly Thr Glu Asn Glu Phe Phe
    275                 280                 285

Thr Leu Glu Gln Leu Val Glu Lys Phe Thr Ile Glu Arg Val Asn Lys
    290                 295                 300

Ser Gly Ala Ile Phe Asp Ser Thr Lys Leu Arg Trp Met Asn Gly Gln
305                 310                 315                 320

His Leu Arg Ser Leu Pro Ser Glu Glu Leu Asn Arg Ile Ile Gly Glu
            325                 330                 335

Arg Trp Lys Asp Ala Gly Ile Ala Thr Glu Ser Gln Gly Ile Phe Ile
            340                 345                 350

Gln Asp Ala Val Leu Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp
            355                 360                 365

Ser Glu Lys Ala Leu Ser Ser Leu Leu Ser Tyr Pro Leu Tyr Glu Thr
    370                 375                 380

Leu Ala Ser Ala Glu Gly Lys Pro Ile Leu Glu Asp Gly Val Ser Glu
385                 390                 395                 400

Val Ala Lys Ser


<210> 15
<211> 407
<212> DNA
<213> Triticum aestivum

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<222> (14)
<223> n = A, C, G or T

<220>
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<220>
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gcaaggacgc gattcgcgcc gtcaccaaca gggaatcttc atcttggttc cctacgtacg 180
gccctcttca attacctgat tgcaaaagct acacgcggta aattcatcct acgcatagag 240
gacacagatn agtcaaggac tgttcctggt gcgattgaaa aactctgcgc tgntttgaga 300
tggggggtt taaaaaggga taaaagggct ggtccccaat ngaccgcaan ngggcctttc 360
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<210> 16
<211> 79
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (55)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (69)
<223> Xaa = ANY AMINO ACID

<400> 16
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Ala Pro Ser Pro Thr Gly Asn Leu His Leu Gly Ser Leu Arg Thr Ala
            20   25   30

Leu Phe Asn Tyr Leu Ile Ala Lys Ala Thr Arg Gly Lys Phe Ile Leu

16

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      35   40   45

Arg Ile Glu Asp Thr Asp Xaa Ser Arg Thr Val Pro Gly Ala Ile Glu
    50   55   60

Lys Leu Cys Ala Xaa Leu Arg Trp Gly Gly Leu Lys Arg Asp Lys
    65   70   75
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<210> 17
<211> 2387
<212> DNA
<213> Zea mays

<400> 17

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gcgggcgctg catgtcttaa tgcgcatcga gctcaacgca cccgtcaaat tggggaagag   180
ggatgctggt gaaaccggtg aggggaagga ggaggcactg gtggtgctgg ccacacagct   240
cgctagagca gtgcaggcac tcagcaagct gagcattgcc cgggcacggc tctgtgcgga   300
gagtattgct gatgctgagc ttcgggagaa gcttactggt ggcgttagcg ttgatgattt   360
gaaggggatg cttgacaatg ttttgattga ttcagatgcc gtatcagtct tgaaggggt   420
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caagatgcat ggtgctactg cgcttgatac acccgtattt gagctgagag aaacccttat   960
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atcaagcatt ccgtggatgg tgctagtcgg cgagtctgag ctgcagaaag aactgtaaa   2040
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<210> 18
<211> 495
<212> PRT
<213> Zea mays

<400> 18

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Met Leu Leu Arg Asp His Val Thr Asn Gly Ser Thr Val Ala Ala Met
  1               5                  10                  15

Asn Ser Ala Ser Val Ala Glu Trp Ala Thr Ser Leu Ser Leu Leu Phe
             20                  25                  30

Asp Pro Lys Cys Pro Gly Leu Glu Ser Leu Val Glu Lys Val Lys Glu
         35                  40                  45

Ile Val Glu Ser Asn Glu Val Arg Arg Leu Pro Lys Ile Pro Lys Gly
     50                  55                  60

Thr Arg Asp Phe Gly Lys Glu Gln Met Ala Ile Arg Glu Arg Ala Phe
 65              70                  75                      80

Ser Ile Ile Thr Ser Val Phe Lys Met His Gly Ala Thr Ala Leu Asp
             85                  90                  95

Thr Pro Val Phe Glu Leu Arg Glu Thr Leu Met Gly Lys Tyr Gly Glu
         100                 105                 110

Asp Ser Lys Leu Ile Tyr Asp Leu Ala Asp Gln Gly Gly Glu Leu Cys
         115                 120                 125

Ser Leu Arg Tyr Asp Leu Thr Val Pro Phe Ala Arg Tyr Val Ala Met
     130                 135                 140

Asn Ser Ile Ser Ala Leu Lys Arg Tyr Gln Ile Ala Lys Val Tyr Arg
145                 150                 155                 160

Arg Asp Asn Pro Ser Lys Gly Arg Tyr Arg Glu Phe Tyr Gln Cys Asp
             165                 170                 175

Phe Asp Ile Ala Gly Val Tyr Glu Pro Met Glu Pro Asp Phe Glu Val
         180                 185                 190

Ile Lys Val Leu Thr Glu Leu Leu Asn Gln Leu Asp Ile Gly Thr Tyr
         195                 200                 205

Glu Ile Lys Leu Asn His Arg Lys Leu Leu Asp Gly Met Leu Glu Ile
     210                 215                 220

Cys Gly Val Pro Pro Gln Lys Phe Arg Thr Val Cys Ser Ser Ile Asp
225                 230                 235                 240

Lys Leu Asp Lys Gln Thr Phe Glu Gln Val Lys Lys Glu Leu Val Asp
             245                 250                 255

Glu Lys Gly Ile Ser Asn Glu Thr Ala Asp Glu Ile Gly Asn Leu Val
             260                 265                 270

Lys Thr Arg Gly Pro Pro Leu Glu Val Leu Met Glu Leu Arg Lys Glu
         275                 280                 285

Gly Ser Lys Phe Met Asn Asn Val Gly Ser Val Ala Ala Leu Asn Glu
     290                 295                 300

Leu Glu Ile Leu Phe Lys Ala Leu Asp Lys Ala Asn Ala Ile Ser Lys
305                 310                 315                 320

Ile Thr Phe Asp Leu Ser Leu Ala Arg Gly Leu Asp Tyr Tyr Thr Gly
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18

Val Ile Tyr Glu Ala Val Phe Lys Gly Ala Ala Gln Val Gly Ser Ile
            340   345   350

Ala Ala Gly Gly Arg Tyr Asp Asn Leu Val Gly Met Phe Ser Gly Lys
            355   360   365

Gln Ile Pro Ala Val Gly Val Ser Leu Gly Ile Glu Arg Val Phe Ala
            370   375   380

Ile Met Glu Gln Gln Glu Lys Glu Arg Asn Glu Lys Ile Arg Pro Thr
385   390   395   400

Glu Thr Glu Val Leu Val Ser Ile Leu Gly Lys Asp Leu Thr Leu Ala
                405   410   415

Ala Glu Leu Val Ser Glu Leu Trp Asn Ala Gly Ile Lys Ala Glu Phe
            420   425   430

Lys Leu Thr Thr Arg Val Ala Asn His Ile Lys Tyr Ala Leu Gln Ser
            435   440   445

Ser Ile Pro Trp Met Val Leu Val Gly Glu Ser Glu Leu Gln Lys Gly
    450   455   460

Thr Val Lys Leu Lys Asp Val Glu Ala Asn Gln Glu Glu Glu Val Asp
465   470   475   480

Arg Lys Asp Phe Val Arg Glu Leu Lys Lys Arg Leu Ser Lys Ser
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<213> Glycine max

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gtcgaaaggt tctgcaagaa gtattaaatt gttattcagt accagaaaat ttatttggca  180
aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt  240
tgaaagctgt tggtctatct caagaggctg tccaggagct attgcaagtc ctttctgtga  300
agtcattgac cgagttagaa gagagacttg ggagcagtgg ggaagcagtt gctgatctga  360
aacagctatt ctcccttgct gaaaaaattg gttactctaa atggcttcaa tttgatgcat  420
cagttgttcg aggtcttgct tactacactg gcattgtatt tgagggtttt gaccgagaag  480
gaaagctgcg agctatctgt ggtggtggtc gatatgatca tttgttctca acttttggtg  540
ctgatgacat tgctgcatgt ggttttggat ttggtgatgc aagtcatagt ggaattgctc  600
aaaagagaan ggtctgttac cgggaagctt aacttgcaaa tagatgacat tgtgtgtgcc  660
ttggaccaaa gatcttcaag ggatgtgctg ctatgggccc caacaatctc agngaaaaan  720
ggcaaattgt tgaagttggn tttgggaaaa caaa                                754
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<212> PRT
<213> Glycine max

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Ile Ala Ser Ile Val Thr Leu Phe Lys Arg Ile Gly Ile Thr Glu Ser
             20                  25                  30

Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu
         35                  40                  45

Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile
     50                  55                  60

Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu
 65                  70                  75                  80

Lys Ala Val Gly Leu Ser Gln Glu Ala Val Gln Glu Leu Leu Gln Val
                 85                  90                  95

Leu Ser Val Lys Ser Leu Thr Glu Leu Glu Glu Arg Leu Gly Ser Ser
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20

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Gly Glu Ala Val Ala Asp Leu Lys Gln Leu Phe Ser Leu Ala Glu Lys
        115                 120                 125

Ile Gly Tyr Ser Lys Trp Leu Gln Phe Asp Ala Ser Val Val Arg Gly
        130                 135                 140

Leu Ala Tyr Tyr Thr Gly Ile Val Phe Glu Gly Phe Asp Arg Glu Gly
145                 150                 155                 160

Lys Leu Arg Ala Ile Cys Gly Gly Gly Arg Tyr Asp His Leu Phe Ser
                165                 170                 175

Thr Phe Gly Ala Asp Asp Ile Ala Ala Cys Gly Phe Gly Phe Gly Asp
            180                 185                 190

Ala Ser His Ser Gly Ile Ala Gln Lys Arg Xaa Val Cys Tyr Arg Glu
            195                 200                 205

Ala Leu Ala Asn Arg His Cys Val Cys Leu Gly Pro Lys Ile Phe Lys
        210                 215                 220

Gly Cys Ala Ala Met Gly Pro Asn Asn Leu Xaa Glu Lys Xaa Gln Ile
225                 230                 235                 240

Val Glu Val
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<212> DNA
<213> Triticum aestivum

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tgacaagctg gggaaactga gtagggaaga aattgagaag gaattgattt caactgggct  180
gtcatctgaa gcagtacagg gcatcattga agtgctctct ctcaagtcac tgtccaaact  240
tgaagaggtg ctaggctcag gtgttgaagc cgttgctgac ttgaagaagc tcttctcgct  300
tgctgagcaa tatggttatt ctgattggat ctgtttcgat gcatctgttg ttcgtggcct  360
tgcatactac acagggattg tttttgaggc ttttgatagg gaaggggaac tgagagcgat  420
ttgtggtggg gggaggtatg acaggctact gtcaacattt ggaactgaag atgtaccagc  480
ctgtggcttt ggatttggag atgctgtcat agtggagctg ctgaaagaaa agggtctttt  540
gcctgacctg ccacgtcaaa tagatgacat tgtgttccca ttggacgagg agcttgaggg  600
gccagcatct agtgttgcat cctgtctgcg gaagaagggc agatctgtag accttgtaga  660
agacaagcgt ctgaaatggg tgttcaaaca tgctgagagg ataaacgcta gcaggctgat  720
cttggttggg aaatccgagt gggagcgagg catggtccgt gtgaagatac tatcaaccag  780
agaagagttc gaggtcaagg cgggcgaatt gcagtagctg ttagctgatc tggtcgattt  840
gaaggtttga cttgtcccct ttcttctttc tgatcatctt caacactgta agttttgcaa  900
ttcacgtcgt gtatacaaac aattaggtgg ctttgaatgc tattgccatc ttctttcgga  960
tcattcacct tgcaacaaac aaagaaattg taggttttgc cattcaccaa catgtattga 1020
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1140
aaaaaaaaaa aaaaaaaaaa aaaa                                        1164

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<212> PRT
<213> Triticum aestivum
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<400> 22

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Lys Leu Gly Ile Thr Ser Ser Asp Val Gly Ile Arg Leu Ser Ser Arg
 1               5                  10                  15

Lys Val Leu Gln Ala Val Leu Asp Met Tyr Ser Val Pro Gln His Leu
            20                  25                  30

Phe Thr Gln Val Cys Val Ile Val Asp Lys Leu Gly Lys Leu Ser Arg
        35                  40                  45

Glu Glu Ile Glu Lys Glu Leu Ile Ser Thr Gly Leu Ser Ser Glu Ala
    50                  55                  60

Val Gln Gly Ile Ile Glu Val Leu Ser Leu Lys Ser Leu Ser Lys Leu
65                  70                  75                  80

Glu Glu Val Leu Gly Ser Gly Val Glu Ala Val Ala Asp Leu Lys Lys
            85                  90                  95

Leu Phe Ser Leu Ala Glu Gln Tyr Gly Tyr Ser Asp Trp Ile Cys Phe
            100                 105                 110

Asp Ala Ser Val Val Arg Gly Leu Ala Tyr Tyr Thr Gly Ile Val Phe
            115                 120                 125

Glu Ala Phe Asp Arg Glu Gly Glu Leu Arg Ala Ile Cys Gly Gly Gly
    130                 135                 140

Arg Tyr Asp Arg Leu Leu Ser Thr Phe Gly Thr Glu Asp Val Pro Ala
145                 150                 155                 160

Cys Gly Phe Gly Phe Gly Asp Ala Val Ile Val Glu Leu Leu Lys Glu
            165                 170                 175

Lys Gly Leu Leu Pro Asp Leu Pro Arg Gln Ile Asp Asp Ile Val Phe
            180                 185                 190

Pro Leu Asp Glu Glu Leu Glu Gly Pro Ala Ser Ser Val Ala Ser Cys
            195                 200                 205

Leu Arg Lys Lys Gly Arg Ser Val Asp Leu Val Glu Asp Lys Arg Leu
    210                 215                 220

Lys Trp Val Phe Lys His Ala Glu Arg Ile Asn Ala Ser Arg Leu Ile
225                 230                 235                 240

Leu Val Gly Lys Ser Glu Trp Glu Arg Gly Met Val Arg Val Lys Ile
            245                 250                 255

Leu Ser Thr Arg Glu Glu Phe Glu Val Lys Ala Gly Glu Leu Gln
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ttaagagtga tggtggcttc aactatgcct caacagactt aactgctctt tggtatcggc 180
tcaatgttga gcaggcagag tggatcatat atgttacaga tgttggtcag cagcagcact 240
ttgacatggt tttcagtgct gcaaagatgg ccggttggct cccagatcca agtgaaaaga 300
agtttccgaa aacaagccat gttggatttg gtcttgttct tggttcaaga tggcaagcgg 360
ttccgaaccc gcagtactga ggttgttcga ttggtagagc tacttgatga ggctaaatct 420
cggagcaaat cagaactact acaacggctc actgaaaatg gcaaaattgt tgactggacg 480
gatgangaat tagagcaaac ttcagaggct gttggatatg gtgctgtgaa gtacgctgat 540
ctaaaaaata acaggctcac taattacaca tttagttttg aacaaatgct gagcgataag 600
ggaaatactg ctgtgtacct tcagtatgca catgctcgta tttgttccat tattcggaaa 660
tccaacaaga acgtggnaga ctgaagagat ggagccattt ctctcgacca tccggattag 720
cgctgttggg gctgtatctt anccgatttg cagagttgtt gaagaggatc acgaactact 780
ccaaatttgt gtgtgaatac tgtcaatcan ctgaaagtca caanatcata caactgcaag 840
tggtgggtcc ngaggaacac cggtgtgctt gcaacgacgc gtttcatcna agnctcaccg 900
ctcggatacn cat   913

<210> 24
<211> 221

<212> PRT
<213> Zea mays

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Gly Leu Ile Lys Glu Ser Glu Gly Ala Arg Val Ile Phe Ile Gln Gly
            20   25   30

His Gln Ile Pro Leu Ile Val Val Lys Ser Asp Gly Gly Phe Asn Tyr
        35   40   45

Ala Ser Thr Asp Leu Thr Ala Leu Trp Tyr Arg Leu Asn Val Glu Gln
    50   55   60

Ala Glu Trp Ile Ile Tyr Val Thr Asp Val Gly Gln Gln Gln His Phe
65   70   75   80

Asp Met Val Phe Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Asp Xaa
                85   90   95

Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Phe Leu
            100   105   110

Val Gln Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg
        115   120   125

Leu Val Glu Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu
    130   135   140

Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Xaa Glu Leu Glu Gln
145   150   155   160

Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala Asp Leu Lys
                165   170   175

Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Glu Gln Met Leu Ser
            180   185   190

Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala His Ala Arg Ile
            195   200   205

Cys Ser Ile Ile Arg Lys Ser Asn Lys Asn Val Xaa Asp
    210   215   220

24

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ggttttgggg attaccagtg caacaatgct atgagtgtat tttcaagaat aagaggatcc   180
gcaacaaact tccgtaaccc catggcagtt gggcaggcaa ttgcaaataa cctcccccag   240
tcaaatatta tcgaatccat ctctgttgcc gganctggtt acattaacat aacgttatcc   300
agcaattgga ttgcacagag gatacaaaga catgcttggt tgtgggaatc aaaacatggg   360
gaacaatcct taacctgttt aagaaggcaa ntgctggntt tttcaanccc caataattgc   420
aaaaagaana tgcaagttgg gcaataatna aggncaacaa taaatngggg natancccaa   480
ctcaaaangg ttgnggntca caaaanggtt aanttcntcn acgtaaacan gttgggaaac   540
ngggggnacac a   551

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<211> 68
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<213> Oryza sp.

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Arg Gly Ser Ala Thr Asn Phe Arg Asn Pro Met Ala Val Gly Gln Ala
                20   25   30

Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile Ile Glu Ser Ile Ser Val
        35   40   45

Ala Gly Xaa Gly Tyr Ile Asn Ile Thr Leu Ser Ser Asn Trp Ile Ala
    50   55   60

Gln Arg Ile Gln
 65

<210> 27
<211> 411
<212> DNA
<213> Glycine max

<220>
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acaactgatc tagcatcact ttggtatcgt ctaaatgaag aaaaacttga atggattgta 120
tatgttacag atattgggca gcaacagcac tttgatatnc tattnaaggc ctataggcgt 180
gcaggttggt taccaaagga tgagaatgcg tatccaaaat gtactcatat aggttttggt 240
cttgttcttg gggaagatgg aaaacgattt cggactcgca ncagtnangt tgttcgatta 300
gttgattact tgatgaagct aaaangcgct gtaaaattgc cntcttgaaa cgtgatacaa 360
ctaaaggatt ggnctgaagg aggagatcga gaaaacatcc gaagcagttg g   411

<210> 28
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<213> Glycine max

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Val Glu Gly Val Asp Xaa Pro Leu Ile Ala Val Xaa Arg Asp Gly Gly
 1               5                  10                  15

Xaa Asn Tyr Phe Thr Thr Asp Leu Ala Ser Leu Trp Tyr Arg Leu Asn
                20                  25                  30

Glu Glu Lys Leu Glu Trp Ile Val Tyr Val Thr Asp Ile Gly Gln Gln
            35                  40                  45

Gln His Phe Asp Xaa Leu Xaa Lys Ala Tyr Arg Arg Ala Gly Trp Leu
        50                  55                  60

Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly
65                  70                  75                  80

Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Xaa Ser Xaa
                85                  90                  95

Val Val Arg Leu Val Asp Tyr Leu Met Lys Leu Lys Xaa Ala Val Lys
            100                 105                 110

Leu Pro Ser
        115

<210> 29
<211> 565
<212> DNA
<213> Triticum sp.

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ctcgtagtac tgaggttgtt cggttgggaa gacctacttg atgaggctaa atctcgaagt   180
aaatcaagaa cttctccaag cgtctcactg gaaaatggta aaattgttga ctggactgat   240
gaaggaacta agagcaaact tcaaaaggca gtaagatatg cgcctgtcaa agtatgcggg   300
tctgaaagaa taaccgactg actaattaca cttcaacttt gattcaagan ctaagtgaca   360
agggaaatac tgctgtcnac ttcaataagc caagcccgta cctcccanca ttcnaaaacc   420
caacatggtg tnnaaaacta aaangatggg anattccncc tgccanccaa atagctgcct   480
gggacgnact aacngtatgc aanatgttaa aaggatgaca acncttccaa tgtcngggng   540
aaactatnac taccnaagta aaagt   565

<210> 30
<211> 33
<212> PRT
<213> Triticum sp.

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  1   5   10   15

Gly Ala Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg
          20   25   30

Leu

<210> 31
<211> 546
<212> DNA
<213> Oryza sp.

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<220>
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<222> (512)
<223> n = A, C, G or T

<400> 31
atcactattt ccccctgatg tactcatcaa gagttttgag gatagatgga aggacacagg   60
cattctccag gagtctgaaa gtggttttgc taaagaagcg gctgagcttt tgaaggatgg   120
catcgatttg atcactgatg ctgacgcagc cctttcaaac ctgttgtcgt atcccctcca   180
tgctacatta agcagtgatg aagctaaatc tgtggtgcaa gacaagcttt ctgaggttgc   240
atcaggactc atttctgctt atgatagcgg tgaactttgt caagcactag ctgagggccg   300
tgatggttgg cagaagtggg tgaaaatttt tggcaaatca cttaaaagaa agggaaagtc   360
actctttatg ccgctccgtg tactgctgac tggcaagctt catgggcctg acatgggcgg   420

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caccgtagtc ctcatacaca aagccggnac tgtggagcgg tcactcaaca atccggtttc 480
gtaaatctcg acgagaggtc agaatcctga angagtggag tggagtcact ggtacaggac 540
aagatc                                                          546
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<210> 32
<211> 147
<212> PRT
<213> Oryza sp.

<400> 32

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Pro Pro Asp Val Leu Ile Lys Ser Phe Glu Asp Arg Trp Lys Asp Thr
  1               5                  10                  15

Gly Ile Leu Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu
             20                  25                  30

Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Ala Leu
         35                  40                  45

Ser Asn Leu Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu
     50                  55                  60

Ala Lys Ser Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu
 65                  70                  75                  80

Ile Ser Ala Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly
                 85                  90                  95

Arg Asp Gly Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys
                100                 105                 110

Arg Lys Gly Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly
             115                 120                 125

Lys Leu His Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys
         130                 135                 140

Ala Gly Thr
145
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<210> 33
<211> 524
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (386)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (423)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (459)
<223> n = A, C, G or T

<220>

<221> unsure
<222> (481)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (483)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (486)
<223> n = A, C, G or T

<400> 33
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accactctca cacccctcgc accttcttct tccaacgacg ccgtttctca gtctctgctc 120
tctccgaaca accaccaccc gttcgcgttc gtttcgctcc ttctcccacc ggaaacctcc 180
acgtcggcgg tgcccgaacg gccctcttca actacttgtt cgcaaggtcc aaaggtggga 240
aatttgtgct gagaattgag gacactgact tggagaggtc caagtaggga gtctgaggag 300
gccatgctca aagatctttc ttggcttgga cttgattggg atgaagggcc tgggtgttgg 360
aggggattat ggtccttaaa aggcantctg agaaggaatt ccttatacaa acaatatgcc 420
ggngaaacta cacaaatccg ggcaagttta accgctgcnt tctggtccaa agagggaact 480
nanagnaaat gaaaggaggt tgctaaacta aagcaactgg cccc   524

<210> 34
<211> 94
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (63)
<223> Xaa = ANY AMINO ACID

<400> 34
Gln Arg Arg Arg Phe Ser Val Ser Ala Leu Ser Glu Gln Pro Pro Pro
 1   5   10   15

Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly
            20   25   30

Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly
        35   40   45

Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Xaa Ser
    50   55   60

Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu
65   70   75   80

Asp Trp Asp Lys Gly Leu Gly Val Gly Gly Asp Tyr Gly Pro
                85   90

<210> 35
<211> 506
<212> DNA
<213> Glycine max

<220>
<221> unsure

33

<222> (18)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (483)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (505)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (506)
<223> n = A, C, G or T

<400> 35
ggaacatgga tattattngt gttcccgggg ttatggctga agcagagctt atagcttcta 60
tcgtcacttt gtttaagcga ataggaatta cagaatcaga tgtcggattt aaggtttcca 120
gtcgaaaggt tctgcaagaa gtattaaatt gttattcagt accagaaaat ttatttggca 180
aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt 240
tgaaagctgt tggtctatct caagaggctg tccaggagct attgcaagtc ctttctgtga 300
agtcattgac cgagttagaa gagagacttg ggagagtggg gaagcagttg ctgatctgaa 360
acagtattct cccttgctga aaaaattggt tactctaaat ggttcaattt gatgatagtt 420
gttcgaggtc ttgcttacta cactggcatt gatttgaggg tttgacgaga ggaagctgca 480
gcntctgtgt gtgtcaatac attgnn   506

<210> 36
<211> 48
<212> PRT
<213> Glycine max

<400> 36
Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu
 1   5   10   15

Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile
                20   25   30

Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu
            35   40   45

<210> 37
<211> 577
<212> DNA
<213> Triticum sp.

<220>
<221> unsure
<222> (140)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (370)
<223> n = A, C, G or T

<220>
<221> unsure

<222> (411)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (413)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (469)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (481)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (504)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (575)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (530)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (551)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (556)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (564)
<223> n = A, C, G or T

<400> 37
cttgggatta catcttctga tgtgggggatc agactgtcca gccgaaaggt tctacaggcc   60
gtgttggata tgtactccgt accacaacac ttgtttactc aagtttgtgt tattgttgac 120
aagctgggga aactgagtan ggaagaaatt gagaaggaat tgatttcaac tgggctgtca 180
tctgaagcag tacagggcat cattgaagtg ctctctctca agtcactgtc caaacttgaa 240
gaggtgctag gctcaggtgt tgaagccgtt gctgacttga agaacctctt ctcgcttgct 300
gagcaatatg gttattctga ttggatctgt ttcgatgcat ctgttgttcg tggccttgca 360
tactacacan gggattgttt ttgaggcttt tgatagggaa gggaaactga nancatttgt 420
ggtggggggg aggtatgaca ggctacgtca acatttggaa ctgaagatnt ccaccctgtg 480
nctttggatt tggaatcctg tcanagtgga ctccnaaaga aaggtctttn ctacctgcac 540
tcaaataata nattgntcca ttgncaagac ttggggg   577

<210> 38

<211> 46
<212> PRT
<213> Triticum sp.

<220>
<221> UNSURE
<222> (38)
<223> Xaa = ANY AMINO ACID

<400> 38
Ile Arg Leu Ser Ser Arg Lys Val Leu Gln Ala Val Leu Asp Met Tyr
 1   5   10   15

Ser Val Pro Gln His Leu Phe Thr Gln Val Cys Val Ile Val Asp Lys
             20   25   30

Leu Gly Lys Leu Ser Xaa Glu Glu Ile Glu Lys Glu Leu Ile
         35   40   45